

RAW SEQUENCE LISTING

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Application Serial Number: 10/524,972
Source: PCT
Date Processed by STIC: 2-26-05

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PCT

RAW SEQUENCE LISTING

DATE: 02/26/2005

PATENT APPLICATION: US/10/524,972

TIME: 10:37:39

Input Set : A:\Final sequence list-13173-00007-US.txt

Output Set: N:\CRF4\02262005\J524972.raw

4 <110> APPLICANT: Schopfer, Christel R.
 5 Flachmann, Ralf
 6 Herbers, Karin
 7 Kunze, Irene
 8 Sauer, Matt
 9 Klebsattel, Martin

11 <120> TITLE OF INVENTION: Method for the production of Astaxanthin in flowers of plants

13 <130> FILE REFERENCE: 13173-00007-US

C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/524,972

C--> 15 <141> CURRENT FILING DATE: 2005-02-18

15 <150> PRIOR APPLICATION NUMBER: PCT/EP2003/009102

16 <151> PRIOR FILING DATE: 2003-08-18

18 <150> PRIOR APPLICATION NUMBER: DE 102 38 980.2

19 <151> PRIOR FILING DATE: 2002-08-20

21 <150> PRIOR APPLICATION NUMBER: DE 102 38 978.0

22 <151> PRIOR FILING DATE: 2002-08-20

24 <150> PRIOR APPLICATION NUMBER: DE 102 38 979.9

25 <151> PRIOR FILING DATE: 2002-08-20

27 <150> PRIOR APPLICATION NUMBER: DE 102 53 112.9

28 <151> PRIOR FILING DATE: 2002-11-13

30 <150> PRIOR APPLICATION NUMBER: DE 102 58 971.2

31 <151> PRIOR FILING DATE: 2002-12-16

33 <160> NUMBER OF SEQ ID NOS: 172

35 <170> SOFTWARE: PatentIn version 3.3

38 <210> SEQ ID NO: 1

40 <211> LENGTH: 1771

42 <212> TYPE: DNA

44 <213> ORGANISM: Haematococcus pluvialis

46 <220> FEATURE:

48 <221> NAME/KEY: CDS

50 <222> LOCATION: (166)..(1155)

52 <400> SEQUENCE: 1

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55 aataataaaag agctcaagcg tttgtgcgcc tcgacgtggc cagtctgcac tgccttgaac 120

57 ccgcgagtct cccgccgcac tgactgccat agcacagcta gacga atg cag cta gca 177

58 Met Gln Leu Ala

59 1

61 gcg aca gta atg ttg gag cag ctt acc gga agc gct gag gca ctc aag 225

62 Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala Glu Ala Leu Lys

63 5 10 15 20

65 gag aag gag aag gag gtt gca ggc agc tct gac gtg ttg cgt aca tgg 273

66 Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val Leu Arg Thr Trp

67 25 30 35

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69 gcg acc cag tac tcg ctt ccg tca gaa gag tca gac gcg gcc cgc ccg      321
70 Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp Ala Ala Arg Pro
71              40              45              50
74 gga ctg aag aat gcc tac aag cca cca cct tcc gac aca aag ggc atc      369
75 Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp Thr Lys Gly Ile
76              55              60              65
78 aca atg gcg cta cgt gtc atc ggc tcc tgg gcc gca gtg ttc ctc cac      417
79 Thr Met Ala Leu Arg Val Ile Gly Ser Trp Ala Ala Val Phe Leu His
80              70              75              80
82 gcc att ttt caa atc aag ctt ccg acc tcc ttg gac cag ctg cac tgg      465
83 Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp Gln Leu His Trp
84 85              90              95              100
86 ctg ccc gtg tca gat gcc aca gct cag ctg gtt agc ggc acg agc agc      513
87 Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser Gly Thr Ser Ser
88              105              110              115
90 ctg ctc gac atc gtc gta gta ttc ttt gtc ctg gag ttc ctg tac aca      561
91 Leu Leu Asp Ile Val Val Val Phe Phe Val Leu Glu Phe Leu Tyr Thr
92              120              125              130
94 ggc ctt ttt atc acc acg cat gat gct atg cat ggc acc atc gcc atg      609
95 Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly Thr Ile Ala Met
96              135              140              145
98 aga aac agg cag ctt aat gac ttc ttg ggc aga gta tgc atc tcc ttg      657
99 Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val Cys Ile Ser Leu
100              150              155              160
102 tac gcc tgg ttt gat tac aac atg ctg cac cgc aag cat tgg gag cac      705
103 Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys His Trp Glu His
104 165              170              175              180
107 cac aac cac act ggc gag gtg ggc aag gac cct gac ttc cac agg gga      753
108 His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp Phe His Arg Gly
109              185              190              195
111 aac cct ggc att gtg ccc tgg ttt gcc agc ttc atg tcc agc tac atg      801
112 Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met
113              200              205              210
115 tcg atg tgg cag ttt gcg cgc ctc gca tgg tgg acg gtg gtc atg cag      849
116 Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr Val Val Met Gln
117              215              220              225
119 ctg ctg ggt gcg cca atg gcg aac ctg ctg gtg ttc atg gcg gcc gcg      897
120 Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala
121              230              235              240
123 ccc atc ctg tcc gcc ttc cgc ttg ttc tac ttt ggc acg tac atg ccc      945
124 Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Met Pro
125 245              250              255              260
127 cac aag cct gag cct ggc gcc gcg tca ggc tct tca cca gcc gtc atg      993
128 His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser Pro Ala Val Met
129              265              270              275
131 aac tgg tgg aag tcg cgc act agc cag gcg tcc gac ctg gtc agc ttt      1041
132 Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp Leu Val Ser Phe
133              280              285              290
135 ctg acc tgc tac cac ttc gac ctg cac tgg gag cac cac cgc tgg ccc      1089

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136 Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His His Arg Trp Pro
137          295          300          305
140 ttc gcc ccc tgg tgg gag ctg ccc aac tgc cgc cgc ctg tct ggc cga      1137
141 Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg Leu Ser Gly Arg
142      310          315          320
144 ggt ctg gtt cct gcc tag ctggacacac tgcagtgggc cctgctgcca      1185
145 Gly Leu Val Pro Ala
146 325
148 gctgggcatg caggttgtgg caggactggg tgagggtgaaa agctgcaggc gctgctgccg      1245
150 gacacgctgc atgggctacc ctgtgtagct gccgccacta ggggaggggg tttgtagctg      1305
152 tcgagcttgc cccatggatg aagctgtgta gtggtgcagg gactacaccc acaggccaac      1365
154 acccttgcatg gagatgtctt gcgtcgggag gactgttggg cagtgtagat gctatgattg      1425
156 tatcttaatg ctgaagcctt taggggagcg acacttagtg ctgggcaggc aacgccttgc      1485
158 aaggtgcagg cacaagctag gctggacgag gactcgggtg caggcagggtg aagaggtgcg      1545
160 ggaggggtgt gccacacca ctgggcaaga ccatgctgca atgctggcgg tgtggcagtg      1605
162 agagctgcgt gattaactgg gctatggatt gtttgagcag tctcacttat tctttgatat      1665
164 agatactggt caggcagggtc aggagagtga gtatgaacaa gttgagaggt ggtgcgctgc      1725
166 ccctgcgctt atgaagctgt aacaataaag tggttcaaaa aaaaaa      1771
169 <210> SEQ ID NO: 2
171 <211> LENGTH: 329
173 <212> TYPE: PRT
175 <213> ORGANISM: Haematococcus pluvialis
177 <400> SEQUENCE: 2
179 Met Gln Leu Ala Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala
180 1          5          10          15
183 Glu Ala Leu Lys Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val
184      20          25          30
187 Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp
188      35          40          45
191 Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp
192      50          55          60
195 Thr Lys Gly Ile Thr Met Ala Leu Arg Val Ile Gly Ser Trp Ala Ala
196 65          70          75          80
199 Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp
200      85          90          95
203 Gln Leu His Trp Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser
204      100         105         110
207 Gly Thr Ser Ser Leu Leu Asp Ile Val Val Val Phe Phe Val Leu Glu
208      115         120         125
211 Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly
212      130         135         140
215 Thr Ile Ala Met Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val
216 145         150         155         160
219 Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys
220      165         170         175
223 His Trp Glu His His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp
224      180         185         190
227 Phe His Arg Gly Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met
228      195         200         205

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231 Ser Ser Tyr Met Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr
232      210      215      220
235 Val Val Met Gln Leu Leu Gly Ala Pro Met Ala Asn Leu Leu Val Phe
236 225      230      235      240
239 Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly
240      245      250      255
243 Thr Tyr Met Pro His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser
244      260      265      270
247 Pro Ala Val Met Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp
248      275      280      285
251 Leu Val Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His
252      290      295      300
255 His Arg Trp Pro Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg
256 305      310      315      320
259 Leu Ser Gly Arg Gly Leu Val Pro Ala
260      325
264 <210> SEQ ID NO: 3
266 <211> LENGTH: 1662
268 <212> TYPE: DNA
270 <213> ORGANISM: Haematococcus pluvialis
272 <220> FEATURE:
274 <221> NAME/KEY: CDS
276 <222> LOCATION: (168)..(1130)
278 <400> SEQUENCE: 3
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281 gctatcgacg tggttgtgag cgctcgacgt ggtccactga cgggcctgtg agcctctgcg      120
283 ctccgtcctc tgccaaatct cgcgtcgggg cctgcctaag tcgaaga atg cac gtc      176
284      Met His Val
285      1
287 gca tcg gca cta atg gtc gag cag aaa ggc agt gag gca gct gct tcc      224
288 Ala Ser Ala Leu Met Val Glu Gln Lys Gly Ser Glu Ala Ala Ala Ser
289      5      10      15
291 agc cca gac gtc ttg aga gcg tgg gcg aca cag tat cac atg cca tcc      272
292 Ser Pro Asp Val Leu Arg Ala Trp Ala Thr Gln Tyr His Met Pro Ser
293 20      25      30      35
295 gag tcg tca gac gca gct cgt cct gcg cta aag cac gcc tac aaa cct      320
296 Glu Ser Ser Asp Ala Ala Arg Pro Ala Leu Lys His Ala Tyr Lys Pro
297      40      45      50
299 cca gca tct gac gcc aag ggc atc acg atg gcg ctg acc atc att ggc      368
300 Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr Ile Ile Gly
301      55      60      65
303 acc tgg acc gca gtg ttt tta cac gca ata ttt caa atc agg cta ccg      416
304 Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile Arg Leu Pro
305      70      75      80
307 aca tcc atg gac cag ctt cac tgg ttg cct gtg tcc gaa gcc aca gcc      464
308 Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu Ala Thr Ala
309      85      90      95
311 cag ctt ttg ggc gga agc agc agc cta ctg cac atc gct gca gtc ttc      512
312 Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala Ala Val Phe

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313	100		105		110		115	
315	att gta ctt gag ttc ctg tac act ggt cta ttc atc acc aca cat gac	560						
316	Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp							
317			120		125		130	
319	gca atg cat ggc acc ata gct ttg agg cac agg cag ctc aat gat ctc	608						
320	Ala Met His Gly Thr Ile Ala Leu Arg His Arg Gln Leu Asn Asp Leu							
321			135		140		145	
323	ctt ggc aac atc tgc ata tca ctg tac gcc tgg ttt gac tac agc atg	656						
324	Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp Tyr Ser Met							
325			150		155		160	
327	ctg cat cgc aag cac tgg gag cac cac aac cat act ggc gaa gtg ggg	704						
328	Leu His Arg Lys His Trp Glu His His Asn His Thr Gly Glu Val Gly							
329			165		170		175	
331	aaa gac cct gac ttc cac aag gga aat ccc ggc ctt gtc ccc tgg ttc	752						
332	Lys Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val Pro Trp Phe							
333	180		185		190		195	
335	gcc agc ttc atg tcc agc tac atg tcc ctg tgg cag ttt gcc cgg ctg	800						
336	Ala Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe Ala Arg Leu							
337			200		205		210	
339	gca tgg tgg gca gtg gtg atg caa atg ctg ggg gcg ccc atg gca aat	848						
340	Ala Trp Trp Ala Val Val Met Gln Met Leu Gly Ala Pro Met Ala Asn							
341			215		220		225	
343	ctc cta gtc ttc atg gct gca gcc cca atc ttg tca gca ttc cgc ctc	896						
344	Leu Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala Phe Arg Leu							
345			230		235		240	
347	ttc tac ttc ggc act tac ctg cca cac aag cct gag cca ggc cct gca	944						
348	Phe Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro Gly Pro Ala							
349			245		250		255	
351	gca ggc tct cag gtg atg gcc tgg ttc agg gcc aac agt gag gca	992						
352	Ala Gly Ser Gln Val Met Ala Trp Phe Arg Ala Lys Thr Ser Glu Ala							
353	260		265		270		275	
355	tct gat gtg atg agt ttc ctg aca tgc tac cac ttt gac ctg cac tgg	1040						
356	Ser Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp							
357			280		285		290	
359	gag cac cac agg tgg ccc ttt gcc ccc tgg tgg cag ctg ccc cac tgc	1088						
360	Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu Pro His Cys							
361			295		300		305	
363	cgc cgc ctg tcc ggg cgt ggc ctg gtg cct gcc ttg gca tga	1130						
364	Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala Leu Ala							
365			310		315		320	
367	cctggtccct ccgctggtga cccagcgtct gcacaagagt gtcattgctac aggggtgctgc	1190						
369	ggccagtggc agcgcagtgc actctcagcc tgtatggggc taccgctgtg ccaactgagca	1250						
371	ctgggcatgc cactgagcac tgggcgtgct actgagcaat gggcgtgcta ctgagcaatg	1310						
373	ggcgtgctac tgacaatggg cgtgctactg gggctctggca gtggctagga tggagttaga	1370						
375	tgcattcagt agcgggtggc aacgtcatgt ggatggtgga agtgctgagg ggtttaggca	1430						
377	gccggcattt gagagggcta agttataaat cgcattgctgc tcatgcgcac atatctgcac	1490						
379	acagccaggg aaatcccttc gagagtgatt atgggacact tgtattggtt tcgtgctatt	1550						
381	gtttttattca gcagcagtac ttagtgaggg tgagagcagg gtggtgagag tggagtgagt	1610						
383	gagtatgaac ctgggtcagcg aggtgaacag cctgtaatga atgactctgt ct	1662						

VERIFICATION SUMMARY

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date